

Figure 1. (SEQ ID NO: 1)

CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC 60  
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT 120  
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTGAGCGAAGTTTGTGGGGATT 180  
TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAACTGACTTTCATTTGCAACATG 240  
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA 300  
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAACTGTAGCTTTGGG 360  
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC 420  
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA 480  
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG 540  
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAACAGAAAT 600  
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTGTGAGAATATTTTCAAGACTACATTA 660  
GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC 720  
GGG 723

Figure 2.

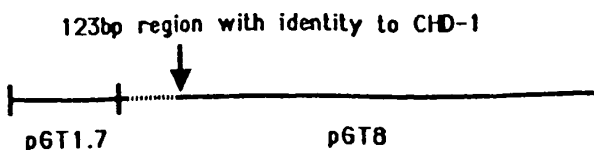


Figure 3.

M CHD-1 ATTCTTCCAG ATGATCCTGA TAAAAACCA CAAGCAAAC AGTTACAGAC (SEQ ID NO: 2)  
 C CHD-1A ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAGC AGCTACAGAC (SEQ ID NO: 3)  
 C CHD-W ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC (SEQ ID NO: 4)  
 GT CHD-W ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAGC AGTTGCAGAC (SEQ ID NO: 5)

M CHD-1 CAAAAACCA CAAGCAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA  
 C CHD-1A CAAGAAACCC CAGGCAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA  
 C CHD-W CAAGAAACCC CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA  
 GT CHD-W CAAGAAACCA CAGGCAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA

M CHD-1 AACTACTTAG CAGAGATCTT GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG  
 C CHD-1A AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAG GCTTGCTGGT GCA  
 C CHD-W AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAG ACTTGCTGGT GCA  
 GT CHD-W AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGTGCABAAG ACTTACTGGT GCA

M CHD-1 ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA (SEQ ID NO: 6)  
 C CHD-1A ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 7)  
 C CHD-W ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 8)  
 GT CHD-W ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA (SEQ ID NO: 9)

\*\*\*\*\*

4080-4083

13

424

Figure 5. (SEQ ID NO: 10)

```

1  CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CCGGCCGGGG
51  AAGGCCTGGC CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT
101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAACATAC
151 GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC
201 TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA
251 AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG
301 GGTCACTTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT
351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC
401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG
451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTGG GAAGTCCAGT
501 CCAAGCATAAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA
551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA
601 GTAGTGAAGA TTCTGCCGAT GATTTCGTCA GTGAACTAA GAAGAAAAAG
651 CATAAAGATG AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC
701 TGGTTCTGAT TCTGAATCGG CGGAAGATGG GGATAAAAGC AGTTGTGAAG
751 AAAGTGAATC TGACTATGAG CCAAAAAACA AAGTCAAAAG CCGTAAACCT
801 CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG GACAGAAGAA
851 GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG
901 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA
951 GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA
1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAAACTATA GAGAAGTTTA
1051 TGGACAGTCG AATTGGCCGA AAAGGAGCCA CTGGTGCCCT AACCACCATC
1101 TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA
1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA
1201 TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA
1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG
1301 CTGGCTGAAA AATGCTTCTC CAGAAGATGT GGAATATTAT AACTGCCAGC
1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAAGAATA
1401 ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG ACTACTATTG
1451 CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGTCT
1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT
1551 CAATCCAAGA CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC
1601 AAGATTTGTT GCACTGAAGA AGCAACCATC TTACATTGGA GGACATGAAA
1651 GTCTGGAGTT AAGAGATTAT CAGTTAAATG GATTGAATTG GCTCGCTCAT
1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGTCTGGG
1751 TAAACCAATA CAAACAATTT CTTTCTGAA CTACCTGTTT CATGAACATC
1801 AACTGTATGG CCTTTTCTT CTGCGCGTGC CACTTCTTAC CTTGACATCT
1851 TGGCAAAGAG AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA
1901 CTTAGGAGAT ATAAGTAGTA GAAATATGAT AAGGACTCAT GAATGGATGC
1951 ATCCACAGAC TAAACGATTA AAGTTTAAAC TACTTCTGAC GACATATGAA
2001 ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT GGGCATTCTAT
2051 AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA
2101 GGAATTAAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC
2151 CCACTGCAAA ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTTCATCAT
2201 GCCAGAAAAA TTTTCTCCTT GGAAGATTTT TGAAGAGGAG CATGGCAAAG
2251 GAAGAGAGTA TGGTTATGCA AGTCTTCACA AAGAGCTTGA ACCATTTTTTA
2301 CTAAGAAGAG TTAAGAAAGA TGTAAGAAAG TCTTTACCTG CTAAGGTTGA
2351 ACAAATCTCG AGGATGGAAA TGAGTGCAAT GCAGAAGCAA TATTACAAGT
2401 GGATTTTAAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTT AAAAGGCAGT
2451 ACCTCAGGCT TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGAACCA
2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATTCTAT AATAAACAGG
2551 AGGCCTTACA GCATTTGATA CGTAGCAGCG GGAAACTAAT CCTTCTTGAC
2601 AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC TGATTTCTC
2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC
2701 AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAGGGGA ATTGAGGAAG
2751 CAAGCACTGG ATCATTTCOA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT
2801 ACTGTCTACA AGAGCTGGAG GATTAGGTAT TAACTTGGCA TCTGCTGACA
2851 CTGTAGTTAT TTTTGATTCT GACTGGAATC CACAGAATGA TCTGCAGGCA
2901 CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA ATATTTATCG
2951 GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA

```

```

3001 AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA
3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA
3101 TAAAGAAGAG TTATCAGCTA TTTTGAAAGT TGGTGCTGAG GAACCTTTTA
3151 AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA
3201 ATCTTGAAGA GAGCTGAAAC TCGGGAAGAT GAGCCAGGTC CATTGACTGT
3251 AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG
3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA
3351 GAAATCATCC CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA
3401 AAAAGAACTT GAAGAAATAT ACATGCTCCC GAGGATGAGA AACTGTGCAA
3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA
3501 TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC GGCCAAAAAA
3551 GCGTGGAAGA CCTCGAACCA TTCTCGAGA AAATATTAAA GGATTAGTGT
3601 ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT
3651 CTGGAAAGGT TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC
3701 TGAGACAGAC CTTAGACGTT TGGGTGAAC TGTACATAAT GGATGCATTA
3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT
3801 GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC
3851 AAACTAGTCT ATCTCTCAGC AAGAAGAGCT GGCACCACTG CACAAATCCA
3901 TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC
3951 AAGGCTGCTC ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT
4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAAA
4051 TGGATCCAGA TCTCAGCTTA ACACAGAAGA TTTTACCTGA TGATCCAGAC
4101 AAGAAACCCC AGGCAAAGCA GCTACAGACT CGTGCAGACT ACCTCATTA
4151 ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAGG CTTGCTGGTG
4201 CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG
4251 GCTTCAAAAA TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCCTC
4301 AGAAAAATCT GATGAAGATG ATGAGGAGGA GGATAACAAG GTAAATGAAA

```

\*\*

```

4351 TGAATCTGA AAATAAGAA AAATCTAAAA AAATTCCATT GCTGGATACT
4401 CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT CAGAAGAATC
4451 TGAAGAACTC CATCAGAAGA CATTAGTGT GTGCAAGAA AGAATGAGGC
4501 CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTTCT
4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA
4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCCGAG CAAATAAAAC
4651 AGTGGAGGAA AAATTTGTGG ATTTTGTGT CCAAGTTTAC AGAATTTGAT
4701 GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAAA AGCGCCAAGA
4751 GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG
4801 TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT
4851 GATAGTAGCA GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA
4901 TGATCATCAC AAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGACT
4951 CCAGGAAAAG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC
5001 TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA GTAAACATAG
5051 AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA
5101 ACTTAAAAGA CAGCCGGGGT CATTGAGATC ACCGCTCCCA TTCAGACCAC
5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC
5201 TTCGAGAGAT TATAGATACC ACTCAGACTG GCAAATGGAC CACAGAGCTT
5251 CTGGTAGTGG CCCGAGGTCA CCACTAGATC AGAGGTCTCC TTATGGTTCA
5301 AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT CAGATCACAA
5351 AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA
5401 CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT
5451 TGCCTTACAT GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT
5501 ATTGTTACTT CTTTCCAGGA TGCAAGGTCT ATTATCCCAA CAGAAGAAAA
5551 ATATTTTGT ATTTAAAGTT TATGCTGCAC TGTGCTGCAA ATGTTGTGGC
5601 ACTTTTTTT TAAGAAATGG AAGATGTTTA CTTTACAGG GACCTCAACA
5651 CTGCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG
5701 TTCTAGGCTG AACACAGATT AAATTATGTT TGTAAATGAA CACTTAAACA
5751 CTGACCTGTG CTTATGTTTC AGGAAAGAA TGGGGATTTA TTTTGTTTTA
5801 TTTCTTGGTA GAGAACTCTC AAGGACTTTG TTCACTTTCC AAAGCTACTT
5851 GTTTACATTG TACACTGCCA CCACCTTGCC GCTTTTCATC ACAAGCTTGA
5901 ATATTTAAAT TCTGTACCTA CAGTTGTAAG ATAGCCAGGA TTTCTCCTGT
5951 TTGTGATCAG TTATAATGCC TTTTATGAA ACAAAACAA ACACATATTA
6001 CAATTAATAA AAAAAACACA ACAAACCAA CAAATGGCTG TAAATTTATG
6051 TAAATTAATT AAATGAGCTT TTTCCGTCA GGCTTTTTTT GGCTGTTCCT
6101 TTCCCAACA ACTCAGGCCT TCTTTTCACA AAGTCAGTAT ACTTACATGT
6151 TTTAATAAAA TATCTCGATG GAATCAGAAT GTAAAAATGG GGAAGGGAAT
6201 ATTTTATTCC ATTTAGTGCT CCTTTTAT TGGATACTTT TACATACCTG
6251 TTTTGGTTG TTTTATTTTA TTTTTTTTT CTATTAAACT GTCAGTGTG
6301 TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAC TGTGCCCTGG
6351 AAAGCTTTTC AGGTGCATTG GTTAAAAAGA AGGAAGTGTT CTATAGGTGA

```

6401 ACACTTCAA ACCCAGATCA GCCAAGATTC ATTGTAAATC CATTGTTTT  
6451 CCTCTTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA  
6501 TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT  
6551 GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAACCAAA  
6601 AAAAAACC

Figure 6.

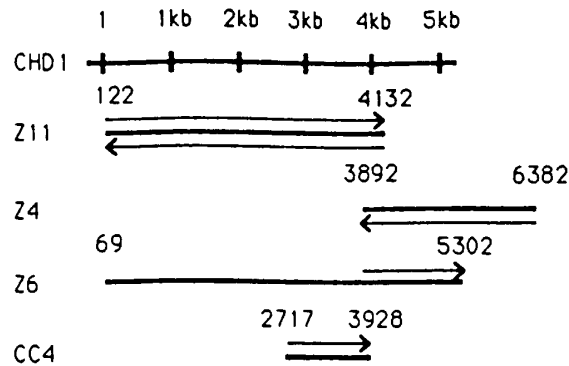


Figure 7.

		D E I V S V K H L H K K I K T E	(SEQ ID NO: 11)
CHD-1A	1	GATGAGATTGTTTCAGTGAACATCTACATAAAAAATAAAAAACAGAAA	(SEQ ID NO: 12)
CHD-W	1	GATGGGATTGTTTCAGTGAACATCCACATAAAAAATAAAAAACAGAAA	(SEQ ID NO: 13)
		D G I V S V K H P H K K I K A E	(SEQ ID NO: 14)
		K E N E E K P E P D I G I K K E A	
CHD-1A	51	AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT	
CHD-W	51	AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT	
		K E N E E K D E P E I G I K K E A	
		E E K R E T K E K E N K R E L K R	
CHD-1A	101	GAAAGAAAAAGAGAGACAAAAGAGAAAGGAAAATAAAAGGGAATTGAAAAGG	
CHD-W	101	GAAGAAAAAGAGAGACAAAAGAGAAAGGAAAATAAAGA	
		G E K R E T K E K E N K	
		E K K E K E D K K E L K E K D N K	
CHD-1A	151	GAGAAAAAGAAAAGAGGATAAGAAAGAATTAAAGAAAAAGATAATAAA	
		E K R E N K V K E S T Q K E K E V	
CHD-1A	201	GAAAAGAGAGAAAAACAAAGTAAAGAATCCACACAGAAAGAAAAAGAAAGTG	
		K E E K	
CHD-1A	251	AAGGAAGAGAAG	

10  
in 157  
9307D

Figure 8. (SEQ ID NO: 15)

```

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA AAGATGGTGT TAGATCATT
10      20      30      40      50      60      70      80
AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA CATAACGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA
90      100     110     120     130     140     150     160
AGGAAGAGTT ATCAGCAATT TTGAAGTTTG GTGCTGAGGA ACTTTTAAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG
170     180     190     200     210     220     230     240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAATC GAGAAAATGA GTCAGGCCCA TTAAGTGTAG GAGATGAGTT
250     260     270     280     290     300     310     320
ACTTTCACAG TTCAAGGTAG CTAAGTTTTC CAATATGGAT GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA
330     340     350     360     370     380     390     400
ACTGGGAAGA AATCATTCCA GAAGTTCAGT GCGCAGCAAT AGAGGGGNGG GAAAGACAAA AAGAACTTGA AGAAATATAT
410     420     430     440     450     460     470     480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA TGCAGTAGGA GCAGAAGATA
490     500     510     520     530     540     550     560
TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCCTGAAA
570     580     590     600     610     620     630     640
ACATTAAAGG ATTTAGTGAT GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCACT TGAAAGGTTA
650     660     670     680     690     700     710     720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGCTCG GGAGAAGTTG TACATAATGG
730     740     750     760     770     780     790     800
ATGCATTAAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA AGAACAGGTG GTAGATTGGG GAAAGTTAAA GGCCCAACAT
810     820     830     840     850     860     870     880
TCCGAATAGC AGGAGTGCGAG GTGAATGCAA AGCTAGTCAT TTCTCAGCAA GAAGAGTTGG CACCATTTGA TAAATCGATT
890     900     910     920     930     940     950     960
CCTTCAGATC CAGAAGAAGG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT TTTGATATAG ATTGGGGTAA
970     980     990     1000    1010    1020    1030    1040
AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT GGTATGGCAA GTTGGGAAAT GATAAAATG GATCCTGATC
1050    1060    1070    1080    1090    1100    1110    1120
TCAGTTTGAC ACAGAAGATT TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC
1130    1140    1150    1160    1170    1180    1190    1200
CTCATTAAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA GGCAATTCAA AGAGGAGAAA
1210    1220    1230    1240    1250    1260    1270    1280
AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC
1290    1300    1310

```

Figure 9.

C CHD-1A DARRYLGNLGH\*RIASQTHYFENIRSTRKGILOLHLVT\*VDLFNLLLTNGHSEDEE (SEQ ID NO: 16)  
 M CHD-1 FALCPFVTQREPQETRECRKFIIEILIFEICITHLLLLIGDPCFINFLIFTHNGHSEDEE (SEQ ID NO: 17)  
 \*\*\*\*\*

C CHD-1A SVRNSSGESRRSDDDSAGSAGSGSGSSSGSSSDGSSSQSGSSDSZSGSESGSQSESESD  
 M CHD-1 SVRNSSGESRRSDDDSAGSAGSGSGSSSGSSSDGSSSQSGSSDSZSGSESGSQSESESD  
 \*\*\*\*\*

C CHD-1A TSREKKQVQAKPPKADGSEFWKSSPSILAVQSAVLKKQOOO---QKAASSDSGSEEDSS  
 M CHD-1 TSRENK-VQAKPPKVDGAEPWKSSPSILAVQSAVLKKQOOO---QKAASSDSGSEEDSS  
 \*\*\*\*\*

C CHD-1A SSEDSDSSSETKKKKKDEDDWQMSGSGSVSGTGSDESAEDGDKSSCEESESDYEPKN  
 M CHD-1 SSEDSDSSSETKKKKKDEDDWQMSGSGSVSGTGSDESAEDGDKSSCEESESDYEPKN  
 \*\*\*\*\*

C CHD-1A KVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEEDDDYDKRGSRRQATVNVSYKEAEZ  
 M CHD-1 KVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEEDDDYDKRGSRRQATVNVSYKEAEZ  
 \*\*\*\*\*

C CHD-1A TKTDSDLLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF  
 M CHD-1 MKTDSDLLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF  
 \*\*\*\*\*

C CHD-1A KTXEHCZIQYLKWKGWSHIHNTWETETLKQONVRCMKLDNYKKQDQETKRWLNAS  
 M CHD-1 EKSKELGEIQYLKWKGWSHIHNTWETETLKQONVRCMKLDNYKKQDQETKRWLNAS  
 \*\*\*\*\*

HUMAN PEDVEYINCQQLTDDLEKQYQIVERTNXSFQSKSAAGYP (SEQ ID NO: 18)  
 C CHD-1A PEDVEYINCQQLTDDLEKQYQIVERI IAHSNQKSAAGYPDYCKWQGLPYSECSWEDGA  
 M CHD-1 PEDVEYINCQQLTDDLEKQYQIVERI IAHSNQKSAAGLPDYCKWQGLPYSECSWEDGA  
 \*\*\*\*\*

C CHD-1A LIAKQFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKQPSYIGGHELELRDYQLN  
 M CHD-1 LISKQFQTCIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKQPSYIGGHELELRDYQLN  
 \*\*\*\*\*

C CHD-1A GLNWLASHWCKGNSCILADEMGLKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWOR  
 M CHD-1 GLNWLASHWCKGNSCILADEMGLKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWOR  
 \*\*\*\*\*

C CHD-1A EIQTWAPQMNNAVYLGDIITSRNMIRTHEWHEPQTKRLKFNILLTTYEILLKDKSFLGGLN  
 M CHD-1 EIQTWASQMNNAVYLGDIITSRNMIRTHEWHEPQTKRLKFNILLTTYEILLKDKSFLGGLN  
 \*\*\*\*\*

C CHD-1A WAFIGVDEAHLKNDOSLLYRTLIDFKSNHRLITGTPLQNSLKLWLSLEFIMPEKFS  
 M CHD-1 WAFIGVDEAHLKNDOSLLYRTLIDFKSNHRLITGTPLQNSLKLWLSLEFIMPEKFS  
 \*\*\*\*\*

C CHD-1A WEDFEEHKGREYGYASLEKELEPFLRRVKKDVEKSLPAKVEQILRMEMSALQKQYK  
 M CHD-1 WEDFEEHKGREYGYASLEKELEPFLRRVKKDVEKSLPAKVEQILRMEMSALQKQYK  
 \*\*\*\*\*

C CHD-1A WILTRNYKALSKSGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNEFYNKQZALQHLIRSS  
 M CHD-1 WILTRNYKALSKSGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNEFYNKQZALQHLIRSS  
 \*\*\*\*\*

C CHD-1A GKLIILLDKLLIRLRERGNRVLIFSQHVRLMILAEYLKYRQPPFORLDGSIKGLRQAL  
 M CHD-1 GKLIILLDKLLIRLRERGNRVLIFSQHVRLMILAEYLKYRQPPFORLDGSIKGLRQAL  
 \*\*\*\*\*



C CHD-1A  
M CHD-1

DBFNAEGSEDFCFLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKKQV  
DBFNAEGSEDFCFLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKKQV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

-IYRLVTGVSVEEDILERAKKXVLDHLVIOQMDTTGKTIVLBTGSTPSSSTPFNKEELSA (SEQ ID NO: 19)  
NIYRLVTGVSVEEDILERAKKXVLDHLVIOQMDTTGKTIVLBTGSAPSSSTPFNKEELSA  
NIYRLVTGVSVEEDILERAKKXVLDHLVIOQMDTTGKTIVLBTGSTPSSSTPFNKEELSA  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

ILKFGAEELFKPEPEEEEEPEQEMDIDEILKRAETRENEGGLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEEEEEPEQEMDIDEILKRAETRENEGGLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEEEEEPEQEMDIDEILKRAETRENEGGLTVGDELLSQFKVANFSNM  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

DEDDIELEPEQNLNWEIIPVQWRRIEGKERQKELEIYMLPRMNCARQISFNGNEG  
DEDDIELEPERNSKNWEIIPVQWRRIEGKERQKELEIYMLPRMNCARQISFNGNEG  
DEDDIELEPERNSKNWEIIPVQWRRIEGKERQKELEIYMLPRMNCARQISFNGNEG  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

RCSRSRRYSGSDSDSISERKRPKGRPRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
RRSRRRYSGSDSDSISERKRPKGRPRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
RRSRRRYSGSDSDSISERKRPKGRPRPTIPRENIGFSDAEIRRFIKSYKFGGPVER  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

LDALARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRGGRFGKVGPTFRISGV  
LDALARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRGGRFGKVGPTFRISGV  
LDALARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRGGRFGKVGPTFRISGV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPYHTKAHFDIDWGEDDSNLLIGIYE  
QVNAKLVLAEDELIPLHKSIPSDPEERKRYVIPYHTKAHFDIDWGEDDSNLLIGIYE  
QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPYHTKAHFDIDWGEDDSNLLIGIYE  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

AGNSKRRKTRSKNKATKAA  
AGGSKRRKTRAKSKAMKSKVKEEIKSDSSPLPSEKSDDEDD----KLNDKSPESKDRS  
AGNSKRRKTRAKSKAMKSKVKEEIKSDSSPLPSEKSDDEDD----KLNDKSPESKDRS  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKSVSDAPVHITASGEFVPIAESEELDQKTFISICKERMRPVKAALKQLDRPEKGLSER  
KKIPLDTPVHITATSEFVPIAESEELDQKTFISICKERMRPVKAALKQLDRPEKGLSER  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EQLHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLHLYKHAI  
EQLHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLHLYKHAI  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKQESQOQNSQON-SNVATTHVIRNPDMERLKENTNEDDSSRDSYSSDRHLSQYHDEHKD  
KKQESQOQNDQNISSNVATTHVIRNPDMERLKENTNEDDSSRDSYSSDRHLSQYHDEHKD  
\*\*\*\*\*

C CHD-1A  
M CHD-1

RHQGDSYKKSRSRKPYSFSGKDHREWDHYRQDSRYYSREKRRKLDHRSREHRPRL  
RHOQDAYKKSRSRKPYSFSGKDHREWDHYRQDSRYYSRS--KRRKLDHRSRDRSRL  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EGGLKD-RCHSDHRSBDSHRSBDSHSTPSTHIIINPRDYRLSDWQDHERAASSGPRSP  
EGNLKDSRGHSDHRSBDSHRSBDSHSTPSTHIIINPRDYRLSDWQDHERAASSGPRSP  
\*\*\*\*\*

C CHD-1A  
M CHD-1

LDQRSYPYGRSP-----FEBSAHERSTPEHTWSSRKTQKLMSSSGTLFXP  
LDQRSYPYGRSPFGHRSPPFEHSSDHSTPEHTWSSRKTQRLTFSGPSFXPYTVNXBSNC  
\*\*\*\*\*

C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A

LTXLERYGLDILSVAVLLLSRMQGLLSQKKNIIVYKVAALCKCCGTTFLNRCGLL  
LQGPQHCPPQTSYYKTLFVQVVLGXTQIKLCLXMTXLTCAVSGKNGGFIIFYFLVE  
NSQGLCSLSKATCLBCTLRPPCRFSSQAXIFKCTYSCKLARIAPVCDQLCLFMKQTNK  
QKTIKKNTTKPTNGCKLLXINXMSFFPSGFWLFLSPTTQAFPSQSYTYHFXNISMZ  
SECKNGEKNILFBLVLLFYWILLBTCPFLFYTFIFFYXTVSVVIVVNSENIPLXTVPVK  
AFQVWFKRRKCSIGZBFTQISQDSLXIHFLSLFMGNNVKCAMQQLIFKXIXMTLLTE  
LLQCTLIVHRXLLSDKLNKPKPT

**Figure 10.**

55	KPPKADGSEFWKSSPSILAVQRSFAVLKQOQQQKSAASDSSGSEEDSSSE	104 (SEQ ID NO: 20)
2654	MAAKDISTEVLQN.PELYGLRRS...HRAAAHQQNYFNDSDDDD...E	2695 (SEQ ID NO: 21)
105	DSADSSSETKKKKHKDEDWQMSGSGSVSGTGSDESAEDGKSSCEESE	154
2696	DNKQSRKRMTTIEDDED.....EFEDEEGEEDSGEDEDEEDFEEDD	2738
155	SDYEPKNKVSRKPPSRIPKPSGKSTGQKKRQLDSSEEEEDDEDYDKR	204
2739	DYYGSPKQNRSKPKSRTKSKSKPKSQSEKQSTVKIP.....TRF	2780
205	GSRRQATVNVSYKEAETKTDSDDLLE...VCGEDVPQT...EDEFE	246
2781	SNRQNKTVNYNIDYSDDDLLESEDDYGSEALSEENVHEASANPQPEDFH	2830
247	TIEKFMSRIGRKATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKW	296
2831	GIDIVINRL.....KTSLEEGKVLEKTVPLNCKE..NYEFLIKW	2870
297	KGWSHIHNTWETEETLKQONVKGMNKLDNYKKK...DQETKRWLKNASPE	343
2871	TDESHLHNTWETYESIGQ..VRGLKRLDNYCKQFIIEDQQVRLDPYVTAE	2918
344	DVEYYNCQQLTDDLHKQYQIVERIIA..HSNQKSAAGYPDYCKWQGLP	391
2919	DIEIMDMERERRLDEFEEFHVPERIIDSQRASLEDGTSQQLYLVKWRRLN	2968
392	YSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALK	441
2969	YDEATWENATDIVKLAPEQVKHFNRENKILPQYSSNYTSQRPFEKLS	3018
442	KOPSYIGGHESLELRDYQLNGLNWLHNSWCKGNSCILADEMGLKGTIQT	491
3019	VQPPFIKGG...ELRDPQLTGINWMAFLWSKGDNGILADEMGLKGTVQTV	3065
492	SFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNNAVYLGDIS	541
3066	AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWAPDLNCICYMGNQKS	3115
542	RNMIRTHEW...MEPQTKRLKFNILLTTYEILLKDKSFLGGLNWFAGIV	587
3116	RDITREYEFYTNPRAGKTKMKNVLLTTYEYILKDRALGSIKWQFMAV	3165
588	DEAHLKNDSDLLYRTLIDFKSNHRLITGTPLQNSLKELWSLLHFMPE	637
3166	DEAHLKNAESSLYESLNSPKVANRMLITGTPLQNNIKELAAALVNFLMPG	3215
638	KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRVKKDVEKSLPAKVEQ	686
3216	RFTIDQEI DFENQDEEQEYIHDLHRRIQPFILRLKKDVEKSLPSKTER	3265
687	ILRMEMSALQKQYKWLTRNYKALSKGSGTSGFLNIMMELKKCCNHC	736
3266	ILRVESDVQTEYKYNILTKNYSALTAGAKGGHFSLLNIMNELKKASNEP	3315
737	YLIKPPDDNEF.....YNKQZALQHLIRSSGKLILLDKLLIRLRERGN	779
3316	YLPDNAEERVLQKFGDGKMTRENVRLGLIMSSGKMVLDDQLLTRLKKDGH	3365

12/18

780 RVLIFSOMVRMLDILAELKYRQFFQRLDGSIKGELRKQALDBFNAEGS 829  
3366 RVLIFSOMVRMLDILGDYLSIKGINFQRLDGTVPQAQRISIDHFNPSDS 3415  
830 EDFCFLSTRAGGLGINLASADTVVIFDSQNDLQQAARAHRIQKK 879  
3416 NDFVFLSTRAGGLGINMTADTVVIFDSQNDLQQAARAHRIQKN 3465  
880 QVNIYRLVTGSGVEEDILERAKKMVLDELVIQMDTTGKTVLHTGSTPS 929  
3466 HVMVYRLVSKDTVEEVLERARKMILEYAIISLGVTDGKNKYTKKNEP.. 3513  
930 SSTPFNKEELSAILKFGAEELFKEPEGEQEPQEMDIDEILKRAETRENE 979  
3514 .....NAGELSAILKFGAGNMFTATD.NQKKLEDNLDDVLNHAEDHVT 3557  
980 PG...PLTVGDELLSQFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR 1026  
3558 PDLGESHGGEFLKQFEVTDY.....KADIDWDDIPEEEL 3594  
1027 RRIEERQKELEE.....IYMLPRMRNCAQI..SFNGSE..... 1060  
3595 KKLQDEEQKRKDEEYVKEQLEMMNRDNALKKIKNSVNGDGTANSDD 3644  
1061 ..GRRSRSSRYSGSDSITERKRPKKRGRPTIPR.ENIKGFS...AE 1104  
3645 DSTSRSSRRRARANDMSIGE...SEVRALYKAILKFGNLKEILDELIAD 3691  
1105 IRRFIKSYKKFGGPLERLDAVARDA.....ELVDKSETDLRRLGEL 1145  
3692 GTLPVKSPFKEYGETYDEMMEAAKDCVHEEKNRKEILEKLEKHATAYRAK 3741  
1146 VHNGCIKALKD.NSSQERAGGRLGKVGPTFRISGVQ.VNAKLVISHEE 1193  
3742 LKSGEIKAEQPKDNPLTRLRLKREKKAFLFNFKGKSLNAESLLSRVE 3791  
1194 ELAPLEKSIPSD.PEERKRYVIPCHTKAA..HFDIDWGKEDDSNLLVGIY 1240  
3792 DLKYLKNLINSNYKDDPLKPSLGNNTPKFVQNWSSNWTKEEDEKLLIGVF 3841  
1241 EYGYGSWEMIKMDPDLSTQKILPDD..... 1266  
3842 KYGYGSWTQIRDDPFLGITDKIFLNEVHNPVAKKSASSDTPTPSKKGK 3891  
1267 .....PDKKPOAKQLQTRADYLIKLLNKDLARK.....EAQRLAGAGNS 1305  
3892 GITGSSKKVPGAIHLGRRVDYLLSFLRGGLNTKSPSADIGSKKLPTGPSK 3941  
1306 KRRKTRNKKNMKASKIKEIKSDSSPQSEKSDDEE...EDNKVNEM 1352  
3942 KRQRKPANHSKSMTEITSSEPANGPPSKRMKALPKGPAALINNTRLSN 3991  
1353 KSENKEKSKIPLLDTPVHITATSEPVPISESEELHQKTFVCKERM RP 1402  
3992 SPTPPLKSKVSRONGTR....QSSNPSSGSAHEKEYDSMDEEDCRBTMSA 4037  
1403 VKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITCLKEYTNPEIQ 1452  
4038 IRTSLKRLRRGGKSLDRKEWAKILKTELTTIGNBI.ESQKGSSRKASPEK 4086  
1453 WRKNLWIFVSKF..TEFDARKLEKLYKBAIKRKQESQ 1488  
4087 YRKELWSYSANFWPADVKSTKLAMY....DKITESQK 4120

Figure 11.

CCHD	AVEAD	GDPNAGFEKSKELGE.IQYLIKWKGWSHIBNTWETEET	LKQQNVKGMNKL DNYKK (SEQ ID NO: 22)
MCHD	AVEAD	GDPNAGFERNKEPGD.IQYLIKWKGWSHIBNTWETEET	LKQQNVKGNKKL DNYKK (SEQ ID NO: 23)
YCHD	EGKVL	EKTVPDLNCKE..N.YEFLIKWTDESHIBNTWETYES	IGQ..VRGLKRL DNYCK (SEQ ID NO: 24)
		****	****
DHP1	EEEE	YAVEKIIDRRVRK.GK.VEYLLKWKGYPETENTWEPENN	LDCQDLIQY (SEQ ID NO: 25)
BHP1	EDEE	YVVEKVLDRRVVKG.QVEYLLKWKGFSEEBNTWEPEKN	LDCPELISEF (SEQ ID NO: 26)
MMOD1	EEEE	YVVEKVLDRRVVKG.GK.VEYLLKWKGFSDENTWEPENN	LDCPDLIAEF (SEQ ID NO: 27)
MMOD2	AEPE	FVVEKVLDRRVVNGK.VEYFLKWKGFADNTWEPENN	LDCPELIEDF (SEQ ID NO: 28)
		****	****
DPC	PVDLV	YAAEKIIQKRVKGV.VEYRVKWKGNQRYNTWEPENN	ILDRRLIDY (SEQ ID NO: 29)
MMOD3	VGEQV	FAAECILSKRLRK.GK.LEYLVKWRGWSSKNSWEPEEN	ILDPRLLLAF (SEQ ID NO: 30)
		****	****
		****	****

Figure 14.

MOUSE	CHD1	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA	(SEQ ID NO: 31)
CHICKEN	CHD-1A	--- --- --- --- --- --- --- ---C ---C --- A-A ---	(SEQ ID NO: 32)
SPIX	CHD-1A	--- --- --- --- --- --- --- ---C ---C --- --- ---	(SEQ ID NO: 33)
CHICKEN	CHD-W	--- --- --- --- --- --- --- ---C ---C --- ---A ---	(SEQ ID NO: 34)
SPIX	CHD-W	--- --- --- --- --- --- --- ---C ---C --- ---A ---	(SEQ ID NO: 35)
HYACINTH	CHD-W	--- --- --- --- --- --- --- ---C ---C --- ---A ---	(SEQ ID NO: 36)
P1		A TAT TCT GGA TCT GAT AGT GAY TC	(SEQ ID NO: 37)
P3		AGA TAT TCC GGA TCT GAT AGT GA	(SEQ ID NO: 38)
MOUSE	CHD1	AGG AAA <u>CGG CCG</u> AAG AAA CGT GGG CGA CCC CGC ACT	
CHICKEN	CHD-1A	--A --- --- --A --A --G --- --A A-- --T --A --C	
SPIX	CHD-1A	--- --- --- --A --A --G --- --A A-- --A --A ---	
CHICKEN	CHD-W	--A --- --A --A --A --- --- --A --- --A --A ---	
SPIX	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---	
HYACINTH	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---	
MOUSE	CHD1	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG	
CHICKEN	CHD-1A	--T --- --A --A --- --- --- --- --- --- --A ---	
SPIX	CHD-1A	--T --- --A --A --- --A --- --- --- --- --- --A ---	
CHICKEN	CHD-W	--T --C --T --A --C --- --- --- --- --- --- --A ---	
SPIX	CHD-W	--T --- --T --A --- --- --- --- --- --- --- ---	
P2		TTT CCT AAA TCG CTA CGT CT	(SEQ ID NO: 39)
HYACINTH	CHD-W	--- --- --- --- --- --- --- ---C --- --A --G	
HYACINTH	CHD-W	ATT AGG CGG T	